

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:20:12 ; Search time 52.2 Seconds

(Without alignments)
37.723 Million cell updates/sec

Title: US-09-331-631A-33

Perfect score: 77
Sequence: 1 CXXCXXCXXXXXXXXXXCXXCXXC 29

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	77	100.0	43	1 SMF2	metallothionein 2
2	77	100.0	143	2 B21761	high cysteine chor
3	77	100.0	152	2 T18975	hypothetical prote
4	77	100.0	164	2 T24272	hypothetical prote
5	77	100.0	188	2 T15651	hypothetical prote
6	77	100.0	273	2 T16246	hypothetical prote
7	77	100.0	314	2 T27686	hypothetical prote
8	77	100.0	325	2 H71271	hypothetical prote
9	68	88.3	55	2 S25774	testis-specific pr
10	68	88.3	63	2 S25772	testis-specific pr
11	68	88.3	68	2 S25775	testis-specific pr
12	68	88.3	68	2 S07807	WDNM1 protein - ra
13	68	88.3	74	2 S25773	testis-specific pr
14	68	88.3	74	2 S61553	probable proteinas
15	68	88.3	87	2 T00564	giberellin-regula
16	68	88.3	93	2 JE0159	giberellin-regula
17	68	88.3	96	2 S43910	giberellin-regula
18	68	88.3	97	2 S71371	giberellin-regula
19	68	88.3	98	2 S60229	giberellin-regula
20	68	88.3	99	2 S60230	giberellin-regula
21	68	88.3	99	2 S60231	giberellin-regula
22	68	88.3	106	2 S60232	giberellin-regula
23	68	88.3	110	2 T49958	GASA4 - Arabidopsi
24	68	88.3	110	1 TITFOR	basic proteinase i
25	68	88.3	112	2 S22151	giberellin-regula
26	68	88.3	112	2 S54832	gip1 protein - gar
27	68	88.3	124	2 T54768	epididymis-specifi
28	68	88.3	125	2 S25454	epididymis-specifi
29	68	88.3	136	2 T36241	hypothetical prote

30	68	88.3	157	1 W5WLR1	E5 protein - rhesu
31	68	88.3	157	2 A25964	thyroglobulin - ra
32	68	88.3	169	1 S18946	ultra high-sulfur
33	68	88.3	182	2 A36686	ultra-high-sulfur
34	68	88.3	191	2 T46412	keratin KAP5.4 - s
35	68	88.3	230	2 A38346	ultra-high-sulfur
36	68	88.3	242	2 G65067	hypothetical prote
37	68	88.3	242	2 T29699	hypothetical prote
38	68	88.3	275	2 T51437	hypothetical prote
39	68	88.3	294	2 T23682	hypothetical prote
40	68	88.3	330	2 T25169	hypothetical prote
41	68	88.3	335	2 T31559	hypothetical prote
42	68	88.3	335	2 T31560	hypothetical prote
43	68	88.3	335	2 T31561	hypothetical prote
44	68	88.3	358	2 T23802	hypothetical prote
45	68	88.3	372	2 T23680	hypothetical prote

ALIGNMENTS

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RESULT 1
SMF2
metallothionein 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #extl_change 24-Nov-1999
C:Accession: S14706; A38808; A29863; S10476
R:Slar, P.; Theodore, L.; Mokdad, R.; Errais, N.E.; Cadic, A.; Megnez, M.
J. Mol. Biol. 215, 217-224, 1990
A:Title: Metallothionein Mto gene of Drosophila melanogaster: structure and regulatio
A:Reference number: S14706; MUID:91012582
A:Accession: S14706
A:Molecule type: DNA
A:Residues: 1-43 <SIL2>
A:Cross-references: EMBL:X52098; NID:g8274; PIDN:CAA36318.1; PID:g295751
A:Accession: A38808
A:Molecule type: protein
A:Residues: 'X', 3-24, 'X', 26-27 <SIL2>
A>Note: 15-Thr was also found
R:Mokdad, R.; Debec, A.; Megnez, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 2658-2662, 1987
A:Title: Metallothionein genes in Drosophila melanogaster constitute a dual system.
A:Reference number: A29863; MUID:87204190
A:Accession: A29863
A:Molecule type: mRNA
A:Residues: 1-43 <MOK>
A:Cross-references: GB:M16250; NID:g157884; PIDN:AA28663.1; PID:g157885
A:Accession:
A:Gene: Mto
A:C:Cross-references: FlyBase:Fgn0002869
A:Map position: 3R 92E
A:introns: 9/1
C:Superfamily: metallothionein
C:Keywords: blocked amino end; chelation; metal binding
F:1/Modified site: blocked amino end (Met) #status experimental

Query Match 100.0%; Score 77; DB 1; Length 43;
Best Local Similarity 20.7%; Pred. No. 17;
Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXCXXC 29
DB 3 CRGCGTNCOCXAKKCGDNCACMKCCVC 31

RESULT 2
B21761
high cysteine chorion B 12 protein precursor - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #extl_change 11-Jan-2000
C:Accession: B21761
R:Ratrou, K.; Tsitlou, S.G.; Kafatos, F.C.
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C:Accession: T27686
R:Thomas, K.
Submitted to the EMBL Data Library, March 1996
A:Reference number: 220404
A:Accession: T27686
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-314 <M1L>
A:Cross-references: EMBL:Z70038; PIDN:CAA9386.1; GSPDB:GN00020; CESP:ZK1067.7
A:Experimental source: clone ZK1067
C:Genetics:
A:Gene: CESP:ZK1067.7
A:Map position: 2
A:Introns: 30/3; 296/2
C:Superfamily: gliadin

Query Match 100.0%; Score 77; DB 2; Length 314;
Best Local Similarity 20.7%; Pred. No. 53;
Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCCCXCC 29
DB 105 CNOCCQCCISSCATPICACSCNMCSSSC 133

RESULT 8
H71271

hypothetical protein TP0856 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: H71271
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; Mcd
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 373-386, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770
A:Accession: H71271
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-325 <COL>
A:Cross-references: GB:AE001256; GB:AE000520; NID:g3323171; PIDN:AAC65828.1; PID:g332317
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0856

Query Match 100.0%; Score 77; DB 2; Length 325;
Best Local Similarity 20.7%; Pred. No. 54;
Matches 6; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCCCXCC 29
DB 238 CKTCGKCTGVCTCCNEKPCCKDCDCNC 266

RESULT 9
S25774

testis-specific protein Mst84dc - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C:Accession: S25774; C56565
R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991
A:Title: A cluster of four genes selectively expressed in the male germ line of Drosophi
A:Reference number: A56565; MUID:92102953
A:Accession: S25774
A:Molecule type: DNA
A:Residues: 1-55 <KUH>
A:Cross-references: EMBL:X67703; NID:g11072; PIDN:CAA47939.1; PID:g11075
A:Note: the authors translated the codon TGC for residue 55 as Thr
A:Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIIP:74222)

C:Genetics:
A:Gene: Mst84dc
A:Cross-references: FlyBase:FBgn0004174
A:Map position: 3
C:Superfamily: fruit fly testis-specific protein
C:Keywords: spermatogenesis; tandem repeat

Query Match 88.3%; Score 68; DB 2; Length 55;
Best Local Similarity 17.9%; Pred. No. 94;
Matches 5; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCCCXCC 28
DB 19 CGPCGPRCPCGCCGCGPCGCGPCG 46

RESULT 10
S25772

testis-specific protein Mst84da - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C:Accession: S25772; A56565
R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991
A:Title: A cluster of four genes selectively expressed in the male germ line of Droso
A:Reference number: A56565; MUID:92102953
A:Accession: S25772
A:Molecule type: DNA
A:Residues: 1-63 <KUH>
A:Cross-references: EMBL:X67703; NID:g11072; PIDN:CAA47937.1; PID:g11073
A:Note: sequence extracted from NCBI backbone (NCBIN:74219, NCBIIP:74224)
C:Genetics:
A:Gene: Mst84da
A:Cross-references: FlyBase:FBgn0004172
A:Map position: 3
A:Introns: 13/3
C:Superfamily: fruit fly testis-specific protein
C:Keywords: spermatogenesis; tandem repeat

Query Match 88.3%; Score 68; DB 2; Length 63;
Best Local Similarity 17.9%; Pred. No. 1e+02;
Matches 5; Conservative 23; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCCCXCC 28
DB 26 CGGCGPCGCGCGCGCGCGCGCGCGT 53

RESULT 11
S25775

testis-specific protein Mst84dd - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C:Accession: S25775; D56565
R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991
A:Title: A cluster of four genes selectively expressed in the male germ line of Droso
A:Reference number: A56565; MUID:92102953
A:Accession: S25775
A:Molecule type: DNA
A:Residues: 1-68 <KUH>
A:Cross-references: EMBL:X67703; NID:g11072; PIDN:CAA47940.1; PID:g11076
A:Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIIP:74223)
C:Genetics:
A:Gene: Mst84dd
A:Cross-references: FlyBase:FBgn0004175
A:Map position: 3
C:Superfamily: fruit fly testis-specific protein
C:Keywords: spermatogenesis; tandem repeat

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Job time: 321 sec
